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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,813

DATE: 02/28/2002

TIME: 10:26:41

Input Set : N:\Crf3\RULE60\10067813.raw.txt

Output Set: N:\CRF3\02282002\J067813.raw

1 <110> APPLICANT: Renault, Jean-Christophe
 2 Louahed, Jamila
 3 Grasso, Luigi
 4 Levitt, Roy
 5 Nicolaides, Nicholas
 6 <120> TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
 7 Atopic Allergies and Related Disorders
 8 <130> FILE REFERENCE: 036870-5071
 9 <140> CURRENT APPLICATION NUMBER: 10/067,813
 10 <141> CURRENT FILING DATE: 2002-02-08
 12 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157,247
 W--> 13 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-18
 14 <160> NUMBER OF SEQ ID NOS: 17
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1119
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Murinae gen. sp.
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (19)..(642)
 24 <400> SEQUENCE: 1

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26	Met Ala Thr Ser Ala Val Pro Ser Glu Asn Leu	
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28	ccc aca tat aaa cta gta gtg gtg gga gat ggt ggt gtg ggc aag agt	99
29	Pro Thr Tyr Lys Leu Val Val Val Gly Asp Gly Gly Val Gly Lys Ser	
30	15 20 25	
31	gcg ctc act att cag ttt ttc cag aag atc ttt gtg cct gac tac gac	147
32	Ala Leu Thr Ile Gln Phe Phe Gln Lys Ile Phe Val Pro Asp Tyr Asp	
33	30 35 40	
34	ccc acc att gaa gac tcc tac ctg aag cat aca gag att gac aat cag	195
35	Pro Thr Ile Glu Asp Ser Tyr Leu Lys His Thr Glu Ile Asp Asn Gln	
36	45 50 55	
37	tgg gcc atc ttg gat gtt ctg gac aca gcc ggg cag gag gag ttc agt	243
38	Trp Ala Ile Leu Asp Val Leu Asp Thr Ala Gly Gln Glu Glu Phe Ser	
39	60 65 70 75	
40	gcc atg cgg gaa caa tac atg cgc aca ggg gat ggc ttc ctc att gtc	291
41	Ala Met Arg Glu Gln Tyr Met Arg Thr Gly Asp Gly Phe Leu Ile Val	
42	80 85 90	
43	tac tcc gtc acc gac aag gcc agc ttc gag cac gtg gac cgc ttc cac	339
44	Tyr Ser Val Thr Asp Lys Ala Ser Phe Glu His Val Asp Arg Phe His	
45	95 100 105	

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46   cag ctc att ctg cgt gtc aag gac agg gag tca ttc cca atg atc ctc   387
47   Gln Leu Ile Leu Arg Val Lys Asp Arg Glu Ser Phe Pro Met Ile Leu
48           110                      115                      120
49   gtg gcc aac aag gtg gat ctg atg cac cta agg aaa gtc acc agg gac   435
50   Val Ala Asn Lys Val Asp Leu Met His Leu Arg Lys Val Thr Arg Asp
51           125                      130                      135
52   caa gga aaa gaa atg gca acc aaa tac aat atc cca tat ata gag acc   483
53   Gln Gly Lys Glu Met Ala Thr Lys Tyr Asn Ile Pro Tyr Ile Glu Thr
54           140                      145                      150                      155
55   agt gcc aag gac ccg cct ctc aac gtg gat aaa acc ttc cat gac cta   531
56   Ser Ala Lys Asp Pro Pro Leu Asn Val Asp Lys Thr Phe His Asp Leu
57           160                      165                      170
58   gtt aga gta att agg caa cag gtt cca gag aaa aac cag aag aag aaa   579
59   Val Arg Val Ile Arg Gln Gln Val Pro Glu Lys Asn Gln Lys Lys Lys
60           175                      180                      185
61   aag aag aca aaa tgg cga gga gac agg gcc acc ggc act cac aaa ctg   627
62   Lys Lys Thr Lys Trp Arg Gly Asp Arg Ala Thr Gly Thr His Lys Leu
63           190                      195                      200
64   cag tgt gtc atc ttg tgacagcctg aagccctggg catagcaacc gtgaactgcc   682
65   Gln Cys Val Ile Leu
66           205
67   agccctggg accagccac tgcctaactg cactgagaac cacttctaac tacagccctt   742
68   ggctcttgga ctgggcattg gaagggaatg agggaggagg gggcagaagc aggccggggc   802
69   tggctttgct gcctgtccca ggagacaggg ctacagcttc caaacctttt gtgtgttgac   862
70   tgagcccagt tcccagtctc ttggtgggct tgtttctttt aactcatagg ctggtttgct   922
71   atggaagtgc ttaccacat acaacgcacc agacaagcca tgagcaagct tcctccctgt   982
72   cccatcccca gtgtctgagc tcttgtgtct tttgtagatt tttaaattat ttgagtaatg  1042
73   attattttat taaagagggtg tgtgccatt gcctgcgaag cccaagtct ttggcagacc  1102
74   tctgataaat gtctgca                                     1119
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77 <211> LENGTH: 208
78 <212> TYPE: PRT
79 <213> ORGANISM: Murinae gen. sp.
80 <400> SEQUENCE: 2
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83   Val Val Val Gly Asp Gly Gly Val Gly Lys Ser Ala Leu Thr Ile Gln
84           20           25           30
85   Phe Phe Gln Lys Ile Phe Val Pro Asp Tyr Asp Pro Thr Ile Glu Asp
86           35           40           45
87   Ser Tyr Leu Lys His Thr Glu Ile Asp Asn Gln Trp Ala Ile Leu Asp
88           50           55           60
89   Val Leu Asp Thr Ala Gly Gln Glu Glu Phe Ser Ala Met Arg Glu Gln
90           65           70           75           80
91   Tyr Met Arg Thr Gly Asp Gly Phe Leu Ile Val Tyr Ser Val Thr Asp
92           85           90           95
93   Lys Ala Ser Phe Glu His Val Asp Arg Phe His Gln Leu Ile Leu Arg
94           100          105          110
95   Val Lys Asp Arg Glu Ser Phe Pro Met Ile Leu Val Ala Asn Lys Val

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96          115          120          125
97  Asp Leu Met His Leu Arg Lys Val Thr Arg Asp Gln Gly Lys Glu Met
98          130          135          140
99  Ala Thr Lys Tyr Asn Ile Pro Tyr Ile Glu Thr Ser Ala Lys Asp Pro
100         145          150          155          160
101  Pro Leu Asn Val Asp Lys Thr Phe His Asp Leu Val Arg Val Ile Arg
102          165          170          175
103  Gln Gln Val Pro Glu Lys Asn Gln Lys Lys Lys Lys Lys Thr Lys Trp
104          180          185          190
105  Arg Gly Asp Arg Ala Thr Gly Thr His Lys Leu Gln Cys Val Ile Leu
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109 <211> LENGTH: 1085
110 <212> TYPE: DNA
111 <213> ORGANISM: Homo sapiens
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113 <221> NAME/KEY: CDS
114 <222> LOCATION: (102)..(725)
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117  ccgagccggg gctggagcgc gcggtctgac ctacgagaaa c atg gcg acc agc gcc 116
118                                     Met Ala Thr Ser Ala
119                                     1 5
120  gtc ccc agt gac aac ctc ccc aca tac aag ctg gtg gtg gtg ggg gat 164
121  Val Pro Ser Asp Asn Leu Pro Thr Tyr Lys Leu Val Val Val Gly Asp
122          10          15          20
123  ggg ggt gtg ggc aaa agt gcc ctc acc atc cag ttt ttc cag aag atc 212
124  Gly Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Phe Phe Gln Lys Ile
125          25          30          35
126  ttt gtg cct gac tat gac ccc acc att gaa gac tcc tac ctg aaa cat 260
127  Phe Val Pro Asp Tyr Asp Pro Thr Ile Glu Asp Ser Tyr Leu Lys His
128          40          45          50
129  acg gag att gac aat caa tgg gcc atc ttg gac gtt ctg gac aca gct 308
130  Thr Glu Ile Asp Asn Gln Trp Ala Ile Leu Asp Val Leu Asp Thr Ala
131          55          60          65
132  ggg cag gag gaa ttc agc gcc atg cgg gag caa tac atg cgc acg ggg 356
133  Gly Gln Glu Glu Phe Ser Ala Met Arg Glu Gln Tyr Met Arg Thr Gly
134          70          75          80          85
135  gat ggc ttc ctc atc gtc tac tcc gtc act gac aag gcc agc ttt gag 404
136  Asp Gly Phe Leu Ile Val Tyr Ser Val Thr Asp Lys Ala Ser Phe Glu
137          90          95          100
138  cac gtg gac cgc ttc cac cag ctt atc ctg cgc gtc aaa gac agg gag 452
139  His Val Asp Arg Phe His Gln Leu Ile Leu Arg Val Lys Asp Arg Glu
140          105          110          115
141  tca ttc ccg atg atc ctc gtg gcc aac aag gtc gat ttg atg cac ttg 500
142  Ser Phe Pro Met Ile Leu Val Ala Asn Lys Val Asp Leu Met His Leu
143          120          125          130
144  agg aag atc acc agg gag caa gga aaa gaa atg gcg acc aaa cac aat 548
145  Arg Lys Ile Thr Arg Glu Gln Gly Lys Glu Met Ala Thr Lys His Asn

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146          135          140          145
147 att ccg tac ata gaa acc agt gcc aag gac cca cct ctc aat gtc gac 596
148 Ile Pro Tyr Ile Glu Thr Ser Ala Lys Asp Pro Pro Leu Asn Val Asp
149 150          155          160          165
150 aaa gcc ttc cat gac ctc gtt aga gta att agg caa cag att ccg gaa 644
151 Lys Ala Phe His Asp Leu Val Arg Val Ile Arg Gln Gln Ile Pro Glu
152          170          175          180
153 aaa agc cag aag aag aag aag aaa acc aaa tgg cgg gga gac cgg gcc 692
154 Lys Ser Gln Lys Lys Lys Lys Lys Thr Lys Trp Arg Gly Asp Arg Ala
155          185          190          195
156 aca ggc acc cac aaa ctg caa tgt gtg atc ttg tgaggcctgc aggcctgaag 745
157 Thr Gly Thr His Lys Leu Gln Cys Val Ile Leu
158          200          205
159 gcctcgggca cagtgcggt ggcctggcca gccctcggga cccctcccca cctaactgca 805
160 ctgaaacat ttctaaccac aacccttggc ccaaggactt ggtacaggaa gggagaaggg 865
161 caggtgggca gggagcaaga caggggtctgg cttttgccaa gaggaacggg gctttttcca 925
162 ccttcttcaa aagagacaag ggaaggccac ctgttaaagc aggaagcagc atcaagttgc 985
163 cccttgggcc ccccatgtt gtttggattt caaaccgggt ttccttcccc cttcttttcg 1045
164 ggttgggtgt tgttggttat ttggttaact acatatggtt 1085
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167 <211> LENGTH: 208
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
170 <400> SEQUENCE: 4
171 Met Ala Thr Ser Ala Val Pro Ser Asp Asn Leu Pro Thr Tyr Lys Leu
172 1 5 10 15
173 Val Val Val Gly Asp Gly Gly Val Gly Lys Ser Ala Leu Thr Ile Gln
174 20 25 30
175 Phe Phe Gln Lys Ile Phe Val Pro Asp Tyr Asp Pro Thr Ile Glu Asp
176 35 40 45
177 Ser Tyr Leu Lys His Thr Glu Ile Asp Asn Gln Trp Ala Ile Leu Asp
178 50 55 60
179 Val Leu Asp Thr Ala Gly Gln Glu Glu Phe Ser Ala Met Arg Glu Gln
180 65 70 75 80
181 Tyr Met Arg Thr Gly Asp Gly Phe Leu Ile Val Tyr Ser Val Thr Asp
182 85 90 95
183 Lys Ala Ser Phe Glu His Val Asp Arg Phe His Gln Leu Ile Leu Arg
184 100 105 110
185 Val Lys Asp Arg Glu Ser Phe Pro Met Ile Leu Val Ala Asn Lys Val
186 115 120 125
187 Asp Leu Met His Leu Arg Lys Ile Thr Arg Glu Gln Gly Lys Glu Met
188 130 135 140
189 Ala Thr Lys His Asn Ile Pro Tyr Ile Glu Thr Ser Ala Lys Asp Pro
190 145 150 155 160
191 Pro Leu Asn Val Asp Lys Ala Phe His Asp Leu Val Arg Val Ile Arg
192 165 170 175
193 Gln Gln Ile Pro Glu Lys Ser Gln Lys Lys Lys Lys Lys Thr Lys Trp
194 180 185 190
195 Arg Gly Asp Arg Ala Thr Gly Thr His Lys Leu Gln Cys Val Ile Leu

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198 <210>	SEQ ID NO: 5		
199 <211>	LENGTH: 19		
200 <212>	TYPE: PRT		
201 <213>	ORGANISM: Homo sapiens		
202 <400>	SEQUENCE: 5		
203	Cys Lys Lys Lys Thr Lys Trp Arg Gly Asp Arg Ala Thr Gly Thr His		
204	1 5 10 15		
205	Lys Leu Gln		
207 <210>	SEQ ID NO: 6		
208 <211>	LENGTH: 24		
209 <212>	TYPE: DNA		
210 <213>	ORGANISM: Murinae gen. sp.		
211 <400>	SEQUENCE: 6		
212	agcactctcc agcctctcac cgca		24
214 <210>	SEQ ID NO: 7		
215 <211>	LENGTH: 12		
216 <212>	TYPE: DNA		
217 <213>	ORGANISM: Murinae gen. sp.		
218 <400>	SEQUENCE: 7		
219	gatctgcggt ga		12
221 <210>	SEQ ID NO: 8		
222 <211>	LENGTH: 24		
223 <212>	TYPE: DNA		
224 <213>	ORGANISM: Murinae gen. sp.		
225 <400>	SEQUENCE: 8		
226	accgacgtcg actatccatg aaca		24
228 <210>	SEQ ID NO: 9		
229 <211>	LENGTH: 12		
230 <212>	TYPE: DNA		
231 <213>	ORGANISM: Murinae gen. sp.		
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233	gatctgttca tg		12
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236 <211>	LENGTH: 24		
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238 <213>	ORGANISM: Murinae gen. sp.		
239 <400>	SEQUENCE: 10		
240	aggcaactgt gctatccgag ggaa		24
242 <210>	SEQ ID NO: 11		
243 <211>	LENGTH: 12		
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245 <213>	ORGANISM: Murinae gen. sp.		
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250 <211>	LENGTH: 18		
251 <212>	TYPE: DNA		
252 <213>	ORGANISM: Murinae gen. sp.		

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,813

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TIME: 10:26:42

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